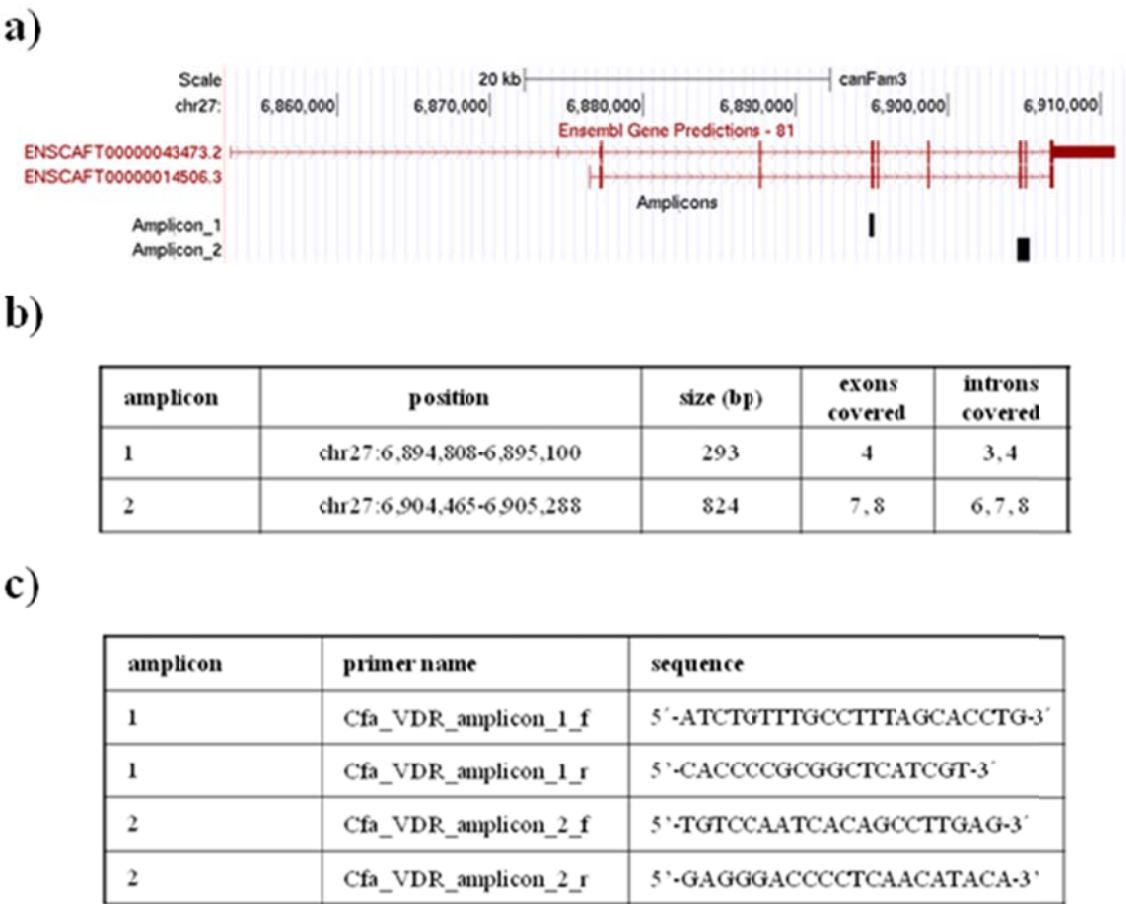


CANINE LEISHMANIASIS IS ASSOCIATED WITH VITAMIN D DEFICIENCY

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SUPPLEMENTARY FIGURES AND TABLES

FIGURE S1. Genomic location of the three amplicons used to identify and genotype genetic variation in the canine VDR gene.



The genomic coordinates are based on the dog genome CanFam3.1/canFam3 assembly.

a) Figure showing the location of the amplicons in relation to the canine VDR exons.

The upper track displays the two known and annotated transcripts of this gene.

b) Table showing genomic location, amplicon size and the exons and introns (on the annotated transcript ENSCAFT00000014506) that are fully or partially covered by these amplicons.

c) Table showing the sequence of each primer from amplicon 1 and amplicon 2.

Table S1. Guide for scoring clinico-pathological signs compatible with canine leishmaniasis

Parameter	Alteration	Score
Weight loss	Normal (no weight loss or the animal grows normally)	0
	Weight loss <10%	1
	Weight loss between 10 and 20%	2
	Weight loss >20%	3
Cutaneous lesions (score for each cutaneous clinical sign: erythema, alopecia,...)	Normal	0
	Slightly generalized (<10% of the body)	1
	Moderately generalized (<25% of the body)	2
	Generalized (>25% of the body)	3
Lymphadenopathy	Absence	0
	Localized	1
	Generalized	2
Renal disorder	Absence	0
	Poliuria	2
Gastrointestinal disorder	Absence	0
	Diarrhoea and/or emesis	2
Splenomegaly	Small increase on spleen size	3
	Large increase on spleen size	5
Ocular	Absence	0
	Slight and Unilateral	1
	Bilateral or severe unilateral	2
	Bilateral and severe	3
Lameness	Absence	0
	Localized	1
	Generalized	2
Epistaxis	Absence	0
	Presence	2
RBC	Normal	0
	Regenerative Anemia	1
	Non-regenerative anemia	2
WBC	Normal	0
	One hematological parameter is altered	1
	Two altered parameters	2
	3 altered parameters	3
	Consecutively	
Proteinogram	Normal	0
	One parameter is altered	1
	Two parameters altered	2
	3 parameters altered	3
	Consecutively	

Table S2. Genotype distribution for each SNP in the three phenotypic classes.

SNP	Genotype	Non-infected (n=15)	Symptomatic (n=11)	Asymptomatic (n=25)
g.6894812A>G	AA	5	4	11
g.6894812A>G	AG	8	1	10
g.6894812A>G	GG	2	2	4
rs851938503 (A>G)	AA	5	7	12
rs851938503 (A>G)	AG	8	1	9
rs851938503 (A>G)	GG	2	3	4
rs852643282 (C>G)	CC	14	10	21
rs852643282 (C>G)	CG	1	1	4
rs852643282 (C>G)	GG	0	0	0
rs852900542 (T>C)	TT	12	10	20
rs852900542 (T>C)	TC	3	1	5
rs852900542 (T>C)	CC	0	0	0